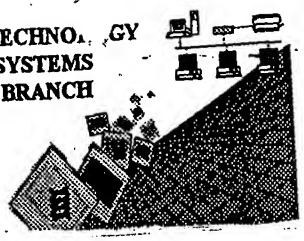
0570
06/9

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/085,233A
Source: OIPE
Date Processed by STIC: 6/17/02

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2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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Revised 01/29/2002

OIPE

Does Not Comply
Corrected Diskette Needed See pg. 7 for explanation of errors

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/085,233A

DATE: 06/17/2002
TIME: 14:46:04

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\06172002\J085233A.raw

```
      3 <110> APPLICANT: YISSUM Research Development Company of the Hewbrew University of
Jerusalem
      5 <120> TITLE OF INVENTION: Fce-PE CHIMERIC PROTEIN FOR TARGETED TREATMENT OF ALLERGY
RESPONSES, A
      6       METHOD FOR ITS PRODUCTION AND PHARMACEUTICAL COMPOSITIONS CONTAINING THE SAME
      8 <130> FILE REFERENCE: 1268-067
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/085,233A
C--> 11 <141> CURRENT FILING DATE: 2002-06-10
     13 <150> PRIOR APPLICATION NUMBER: IL 116436
     14 <151> PRIOR FILING DATE: 1995-12-18
     16 <150> PRIOR APPLICATION NUMBER: PCT / IL96 / 00181
     17 <151> PRIOR FILING DATE: 1996-12-18
     19 <160> NUMBER OF SEQ ID NOS: 8
     21 <170> SOFTWARE: PatentIn version 3.0
     23 <210> SEQ ID NO: 1
     24 <211> LENGTH: 1512
     25 <212> TYPE: DNA
C--> 26 <213> ORGANISM: Artificial
     28 <220> FEATURE:
     29 <223> OTHER INFORMATION: Description of Artificial Sequence: Fce2-3-PE40
     31 <220> FEATURE:
     32 <221> NAME/KEY: CDS
     33 <222> LOCATION: (1)..(1512)
     35 <400> SEQUENCE: 1
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     37 Met Glu Gln Gln Trp Met Ser Glu Ser Thr Phe Thr Cys Lys Val Thr
     38 1               5                  10                  15
     40 tcc caa ggc gta gac tat ttg gcc cac act cgg aga tgc cca gat cat      96
     41 Ser Gln Gly Val Asp Tyr Leu Ala His Thr Arg Arg Cys Pro Asp His
     42             20                  25                  30
     44 gag cca gcc ggt gtg att acc tac ctg atc cca ccc agc ccc ctg gac     144
     45 Glu Pro Ala Gly Val Ile Thr Tyr Leu Ile Pro Pro Ser Pro Leu Asp
     46         35                  40                  45
     48 ctg tat caa aac ggt gct ccc aag ctt acc tgt ctg gtg gtg gac ctg     192
     49 Leu Tyr Gln Asn Gly Ala Pro Lys Leu Thr Cys Leu Val Val Asp Leu
     50     50                  55                  60
     52 gaa agc gag aag aat gtc aat gtg acg tgg aac caa gag aag aag act     240
     53 Glu Ser Glu Lys Asn Val Asn Val Thr Trp Asn Gln Glu Lys Lys Thr
     54 65                  70                  75                  80
     56 tca gtc tca gca tcc cag tgg tac act aag cac cac aat aac gcc aca     288
     57 Ser Val Ser Ala Ser Gln Trp Tyr Thr Lys His His Asn Asn Ala Thr
     58                 85                  90                  95
     60 act agt atc acc tcc atc ctg cct gta gtt gcc aag gac tgg att gaa     336
     61 Thr Ser Ile Thr Ser Ile Leu Pro Val Val Ala Lys Asp Trp Ile Glu
```

62 100 105 110

RAW SEQUENCE LISTING DATE: 06/17/2002
PATENT APPLICATION: US/10/085,233A TIME: 14:46:04

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\06172002\J085233A.raw

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64 ggc tac ggc tat cag tgc ata gtg gac cac cct gat ttt ccc aag ccc      384
65 Gly Tyr Gly Tyr Gln Cys Ile Val Asp His Pro Asp Phe Pro Lys Pro
66         115                 120                 125
68 att gtg cgt tcc atc acc aag acc cca cat atg gcc gaa gag ggc ggc      432
69 Ile Val Arg Ser Ile Thr Lys Thr Pro His Met Ala Glu Glu Gly Gly
70     130                 135                 140
72 agc ctg gcc gcg ctg acc gcg cac cag gct tgc cac ctg ccg ctg gag      480
73 Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu
74 145                 150                 155                 160
76 act ttc acc cgt cat cgc cag ccg cgc ggc tgg gaa caa ctg gag cag      528
77 Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln
78                 165                 170                 175
80 tgc ggc tat ccg gtg cag cgg ctg gtc gcc ctc tac ctg gcg gcg cgg      576
81 Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg
82             180                 185                 190
84 ctg tcg tgg aac cag gtc gac cag gtg atc cgc aac gcc ctg gcc agc      624
85 Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser
86         195                 200                 205
88 ccc ggc agc ggc ggc gac ctg ggc gaa gcg atc cgc gag cag ccg gag      672
89 Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu
90     210                 215                 220
92 cag gcc cgt ctg gcc ctg acc ctg gcc gcc gcc gag agc gag cgc ttc      720
93 Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe
94 225                 230                 235                 240
96 gtc cgg cag ggc acc ggc aac gac gag gcc ggc gcg gcc aac gcc gac      768
97 Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp
98                 245                 250                 255
100 gtg gtg agc ctg acc tgc ccg gtc gcc gcc ggt gaa tgc gcg ggc ccg      816
101 Val Val Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro
102             260                 265                 270
104 gcg gac agc ggc gac gcc ctg ctg gag cgc aac tat ccc act ggc gcg      864
105 Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala
106         275                 280                 285
108 gag ttc ctc ggc gac ggc ggc gac gtc agc ttc agc acc cgc ggc acg      912
109 Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr
110     290                 295                 300
112 cag aac tgg acg gtg gag cgg ctg ctc cag gcg cac cgc caa ctg gag      960
113 Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu
114 305                 310                 315                 320
116 gag cgc ggc tat gtg ttc gtc ggc tac cac ggc acc ttc ctc gaa gcg     1008
117 Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala
118                 325                 330                 335
120 gcg caa agc atc gtc ttc ggc ggg gtg cgc gcg cgc agc cag gac ctc     1056
121 Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu
122             340                 345                 350
124 gac gcg atc tgg cgc ggt ttc tat atc gcc ggc gat ccg gcg ctg gcc     1104
125 Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala
126         355                 360                 365
128 tac ggc tac gcc cag gac cag gaa ccc gac gca cgc ggc cgg atc cgc     1152
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RAW SEQUENCE LISTING DATE: 06/17/2002
PATENT APPLICATION: US/10/085,233A TIME: 14:46:04

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\06172002\J085233A.raw

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    129 Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg
    130     370                 375                 380
    132 aac ggt gcc ctg ctg cgg gtc tat gtc ccg cgc tcg agc ctg ccg ggc     1200
    133 Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly
    134 385                 390                 395                 400
    136 ttc tac cgc acc agc ctg acc ctg gcc gcg ccg gag gcg gcg ggc gag     1248
    137 Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu
    138                 405                 410                 415
    140 gtc gaa cgg ctg atc ggc cat ccg ctg ccg ctg cgc ctg gac gcc atc     1296
    141 Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile
    142             420                 425                 430
    144 acc ggc ccc gag gag gaa ggc ggg cgc ctg gag acc att ctc ggc tgg     1344
    145 Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp
    146         435                 440                 445
    148 ccg ctg gcc gag cgc acc gtg gtg att ccc tcg gcg atc ccc acc gac     1392
    149 Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp
    150     450                 455                 460
    152 ccg cgc aac gtc ggc ggc gac ctc gac ccg tcc agc atc ccc gac aag     1440
    153 Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys
    154 465                 470                 475                 480
    156 gaa cag gcg atc agc gcc ctg ccg gac tac gcc agc cag ccc ggc aaa     1488
    157 Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys
    158                 485                 490                 495
    160 ccg ccg cgc gag gac ctg aag taa                                    1512
    161 Pro Pro Arg Glu Asp Leu Lys
    162             500
    165 <210> SEQ ID NO: 2
    166 <211> LENGTH: 503
    167 <212> TYPE: PRT
C--> 168 <213> ORGANISM: Artificial
W--> 170 <220> FEATURE:
W--> 170 <223> OTHER INFORMATION:
    170 <400> SEQUENCE: 2
    172 Met Glu Gln Gln Trp Met Ser Glu Ser Thr Phe Thr Cys Lys Val Thr
    173 1               5                   10                  15
    176 Ser Gln Gly Val Asp Tyr Leu Ala His Thr Arg Arg Cys Pro Asp His
    177             20                  25                  30
    180 Glu Pro Ala Gly Val Ile Thr Tyr Leu Ile Pro Pro Ser Pro Leu Asp
    181         35                  40                  45
    184 Leu Tyr Gln Asn Gly Ala Pro Lys Leu Thr Cys Leu Val Val Asp Leu
    185     50                  55                  60
    188 Glu Ser Glu Lys Asn Val Asn Val Thr Trp Asn Gln Glu Lys Lys Thr
    189 65                  70                  75                  80
    192 Ser Val Ser Ala Ser Gln Trp Tyr Thr Lys His His Asn Asn Ala Thr
    193                 85                  90                  95
    196 Thr Ser Ile Thr Ser Ile Leu Pro Val Val Ala Lys Asp Trp Ile Glu
    197             100                 105                 110
    200 Gly Tyr Gly Tyr Gln Cys Ile Val Asp His Pro Asp Phe Pro Lys Pro
    201         115                 120                 125
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RAW SEQUENCE LISTING DATE: 06/17/2002
PATENT APPLICATION: US/10/085,233A TIME: 14:46:04

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\06172002\J085233A.raw

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204 Ile Val Arg Ser Ile Thr Lys Thr Pro His Met Ala Glu Glu Gly Gly
205     130                 135                 140
208 Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu
209 145                 150                 155                 160
212 Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln
213                 165                 170                 175
216 Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg
217             180                 185                 190
220 Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser
221         195                 200                 205
224 Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu
225     210                 215                 220
228 Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe
229 225                 230                 235                 240
232 Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp
233                 245                 250                 255
236 Val Val Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro
237             260                 265                 270
240 Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala
241         275                 280                 285
244 Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr
245     290                 295                 300
248 Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu
249 305                 310                 315                 320
252 Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala
253                 325                 330                 335
256 Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu
257             340                 345                 350
260 Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala
261         355                 360                 365
264 Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg
265     370                 375                 380
268 Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly
269 385                 390                 395                 400
272 Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu
273                 405                 410                 415
276 Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile
277             420                 425                 430
280 Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp
281         435                 440                 445
284 Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp
285     450                 455                 460
288 Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys
289 465                 470                 475                 480
292 Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys
293                 485                 490                 495
296 Pro Pro Arg Glu Asp Leu Lys
297             500
300 <210> SEQ ID NO: 3
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RAW SEQUENCE LISTING DATE: 06/17/2002
PATENT APPLICATION: US/10/085,233A TIME: 14:46:04

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\06172002\J085233A.raw

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     302 <212> TYPE: DNA
C--> 303 <213> ORGANISM: Artificial
     305 <220> FEATURE:
     306 <223> OTHER INFORMATION: Description of Artificial Sequence: Fce2-4-PE40
     308 <220> FEATURE:
     309 <221> NAME/KEY: CDS
     310 <222> LOCATION: (1)..(2031)
     312 <400> SEQUENCE: 3
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     314 Met Arg Pro Val Asn Ile Thr Glu Pro Thr Leu Glu Leu Leu His Ser
     315 1               5                  10                  15
     317 tcc tgc gac ccc aat gca ttc cac tcc acc atc cag ctg tac tgc ttc       96
     318 Ser Cys Asp Pro Asn Ala Phe His Ser Thr Ile Gln Leu Tyr Cys Phe
     319             20                  25                  30
     321 att tat ggc cac atc cta aat gat gtc tct gtc agc tgg cta atg gac      144
     322 Ile Tyr Gly His Ile Leu Asn Asp Val Ser Val Ser Trp Leu Met Asp
     323         35                  40                  45
     325 gat cgg gag ata act gat aca ctt gca caa act gtt cta atc aag gag      192
     326 Asp Arg Glu Ile Thr Asp Thr Leu Ala Gln Thr Val Leu Ile Lys Glu
     327     50                  55                  60
     329 gaa ggc aaa cta gcc tct acc tgc agt aaa ctc aac atc act gag cag      240
     330 Glu Gly Lys Leu Ala Ser Thr Cys Ser Lys Leu Asn Ile Thr Glu Gln
     331 65                  70                  75                  80
     333 caa tgg atg tct gaa agc acc ttc acc tgc aag gtc acc tcc caa ggc      288
     334 Gln Trp Met Ser Glu Ser Thr Phe Thr Cys Lys Val Thr Ser Gln Gly
     335                 85                  90                  95
     337 gta gac tat ttg gcc cac act cgg aga tgc cca gat cat gag cca cgg      336
     338 Val Asp Tyr Leu Ala His Thr Arg Arg Cys Pro Asp His Glu Pro Arg
     339             100                 105                 110
     341 ggt gtg att acc tac ctg atc cca ccc agc ccc ctg gac ctg tat caa      384
     342 Gly Val Ile Thr Tyr Leu Ile Pro Pro Ser Pro Leu Asp Leu Tyr Gln
     343         115                 120                 125
     345 aac ggt gct ccc aag ctt acc tgt ctg gtg gtg gac ctg gaa agc gag      432
     346 Asn Gly Ala Pro Lys Leu Thr Cys Leu Val Val Asp Leu Glu Ser Glu
     347     130                 135                 140
     349 aag aat gtc aat gtg acg tgg aac caa gag aag aag act tca gtc tca      480
     350 Lys Asn Val Asn Val Thr Trp Asn Gln Glu Lys Lys Thr Ser Val Ser
     351 145                 150                 155                 160
     353 gca tcc cag tgg tac act aag cac cac aat aac ggc aca act agt atc      528
     354 Ala Ser Gln Trp Tyr Thr Lys His His Asn Asn Gly Thr Thr Ser Ile
     355                 165                 170                 175
     357 acc tcc atc ctg cct gta gtt gcc aag gac tgg att gaa ggc tac ggc      576
     358 Thr Ser Ile Leu Pro Val Val Ala Lys Asp Trp Ile Glu Gly Tyr Gly
     359             180                 185                 190
     361 tat cag tgc ata gtg gac cac cct gat ttt ccc aag ccc att gtg cgt      624
     362 Tyr Gln Cys Ile Val Asp His Pro Asp Phe Pro Lys Pro Ile Val Arg
     363         195                 200                 205
     365 tcc atc acc aag acc cca ggc cag cgc tca gcc ccc gag gta tat gtg      672
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/17/2002
PATENT APPLICATION: US/10/085,233A TIME: 14:46:05

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\06172002\J085233A.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:2,4

VERIFICATION SUMMARY DATE: 06/17/2002
PATENT APPLICATION: **US/10/085,233A** TIME: 14:46:05

Input Set : **A:\pto.vsk.txt**
Output Set: **N:\CRF3\06172002\J085233A.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:26 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:168 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:170 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:170 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:303 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:489 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:491 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:491 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: